

MVPPVLLFLLSSV RATEQPQVVT EHP SMEA ALTGP NASSH FWAN YTFSDW QNFV GRRRYGAESQNPTVKA
ALLIV AY SFTIVF SLFGN VLVC H VIFK NQ RMHSAT SLFIVN LAVADIM ILLNTPFTL VRFVN STWV FGK
MCH VSRFA QYCS LH VSA LTLA IAVDRH QVIMH P LKPRISITKG V IYIAV I WVMATFFS LPHAI CQKLFTF
KYS E DIVR SLCL PDFPE PADL FWK YL DLATF ILLYLLPLF IISVAYARVAKKLWL CNTI G DVTTEQYLA
RHK KTTV KMLV L VVVL FALC WFPL NCYV L LSSKAI HTNNALYFA FHWFAM S STCYN PFIYCWLNENFR
V LK ALLSMC QRPPK PQEDRLP SPVPS F RVAWTEKSHG RRAPL PNHLPSSQI QSGK TDLSS VEPV VAMS
(SEQ ID NO:2)

Figure 1

Underlined = deleted in targeting construct

Bold = sequence flanking Neo insert in targeting construct

GGGGTGGCAGTCGGCACCATCAGGCTCCCTGGCGTTCGGAGTTTCTCTGTGGTCCCG
ACTCTCCGGAGGATCTCGGTTGTCTCCCAAGTCGGAACCTGGCACGGTCCAGGTTCACTC
GGAGGTCCGGGCTTCTCTGTGCCCCCTGCTCCCAGGCTCCCTGTGGTGTG
GACTCCTCTAGCCCCGTGCGCTCAGCCCCCTGCAACCAGCCTCCAGGCACAGAGCCCCGGC
AGGGAGCTCAGCCCCTTGTGCTAGAGCTGCACTGGGTGGACATGAAGGTTCCCTGTCC
TGCTTCTCTTCTCTGTCTCAGTGCAGACTGAGCAACCCAGGTCTGCACTGAGC
ATCCCAGCATGGAGGCAGCCCTGACCGGGCCAACGCCCTCTGCACTTCTGGGCCAACT
ACACTTTCTCTGACTGGCAGAACTTCGTGGCAGGAGACGTTAGGGGCCAGTCCCAGA
ACCCCACGGTGAAGCACTGCTCATGTGGCCTACTCATTACCATGCTCTCGCTCT
TCGGTAATGTCCTGGTCTGTATGTCATTTCAAGAACAGCGCATGCACTGGCCACCA
GCCTCTTCATTGTCAACCTGGCAGTGGCGGACATCATGATCACATTGCTCAACACGCC
TCACTTTGGTCCGCTTGTGAACAGCACATGGGTGTTGGGAAGGGCATGTGTATGCA
GTCGCTTGCTCAGTACTGTTCTACATGTC**CAGCACTGACTCTGACAGCTATCGCAG**
TGGACCGCCACCGAGTCATGCACTGACCTGGATCTCCATCACCAAGGGTG
TCATATATATTGCTGTCATCTGGGTATGGCTACCTCTCTCTGCCCACATGCCATCT
GCCAGAAACTGTTACCTTCAGTACAGTGAGGACATTGTGGCCTCCCTGCCCCTGCGG
ACTTCCCAGGCCAGTGAACCTCTGGAAGTATCTGGACCTGGCCACCTTCATCTGC
TCTACCTACTCCACTTTCAATTATCTCAGTGGCCTATGCTGTGTCACCTGCCCTGCGACGCAAGA
AGAAGACCAACCGTGAAGATGCTGGTGTGGTAGTCCTCTTGCCTCTGCTGGTCC
CTCTCAACTGCTATGTCCTCTTGTCCAGCAAGGCCATCCACACCAACAATGCCCTCT
ACTTTGCTTCCACTGGTTGCCATGAGCAGTACTTGTATAACCCCTCATCTACTGCT
GGCTCAATGAGAACCTTAGGGTTGAGCTTAAGGATTGCTGAGCATGTCACAGGCCAC
CCAAGCCGAGGAAGACAGGCACCCCTCCCCAGTTCTCTCAGGGTGGCATGGACAG
AGAAGACCATGGTCGGAGGGCTCCACTACCTAACCAACTGCCCTCTCCCAGATCC
AGTCTGGGAAGACAGATCTGTCATCTGTGGAACCCGTTGTGGCCATGAGTTAGGAAAGC
TGGAAGTGGTGGGGAGGGTCTTCCCTCTCACAAATTGACCAGACACTAACAGAGTTGG
AAAGTAACACAGAACGACTGAGATGCTGGGTTCTAGGAACCTGTCCAGCCCCATCTGA
TTTGCCTAAACTTTCTAGAAGATGCCATGAGGTGGTGTGTAGATCTTGAGCAAGAGCTC
TGGAAACACCTCAGCTCAACAGAGGCTGGTCCAATCAACCCACCTCCAATTGTGTAGCA
TCTGCCACCTTGCCTTCCACTGCTGAGCAACACAGGGGACTTGAGCCATACTATTG
GTGGGCTGCCCCACATGCTCAGAAAAGAACAGGCACAAAGGTTTCTGAAGTCATTGGA
ACAGGAATAATCACACAGCTTCAGTGAACCTTGGCTCTATCCATGACCAGACAGGCCAT
TTTGGCTCTTAAACAAAGAGAAATTAGTATTGCCACTTTGAAAAGTTCAAGAAAAGTA
AAGAAATGAGTTAGCCCTCAATTGTAAAAAAAGAAAAAAAGAAAAAAAGAAAAAG
AAAGAAAAAAAGCCTGTTAATATGCTGTAAATTATCTGTAGCTTGCCTCTGTGTGT
ACATTGTACTTTAAAATCTGAACACAGTGTCTCATGATGAGATTGTAATAATTAGCAA
GAAACTGGAATATATCAGAGTATTATTGAATTG

Figure 2A

Gene Sequence
Structure *

299 bp Sequence Deleted 753 bp

Size of partial
cDNA: 2253 bp

Targeting Vector* (genomic sequence)

Construct Number: 463

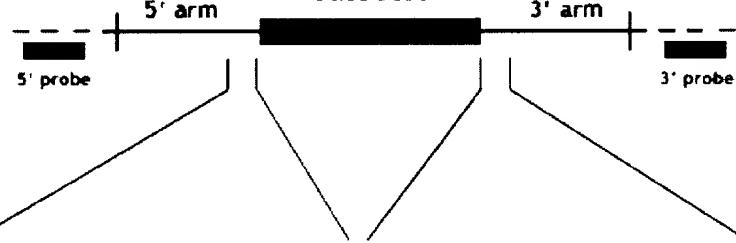
Arm Length:

5': 2.5 kb

3': 0.6 kb

— Targeting Vector
- - - Endogenous Locus

* Not drawn to scale



5' >CTGGCACGGTCCAGGTTCACT
CGGAGGCCGGGCTTCCCTCTGTGC
CCCCTGCCCTCGCTCCCTGGCTC
CCTCTGTGGTGTGGACTCCTCTAG
CCCGGTGCGCTCAGCCCCCTCGCAC
CCAGCCTCCAGGCACAGAGCCCCGG
CAGGGAGCTCAGCCCCTTGTGCCTA
GAGCTGCACTGGCTGGACATGAAG
GTTTCTCCTGT<3'
(SEQ ID NO:3)

5' >CAGCACTGACTCTGACAGCTA
TCGCAGTGACCGCCACCAGGTGA
GAGCACCTGTCCCCCAGCAGCATGC
TCCCATCTCCGTCTATGCCTGGCT
GGCTGGTGGAAATACTGCCACAC
GGTCTGTAGGGAATACTCTCAGGA
CAGTGACTCATTCACTCCGCTGA
CAGCGTGTGTGCTTGCCCTCTGT
TGATCAATTG<3'
(SEQ ID NO:4)

Figure 2B